

SEQUENCE LISTING

<110> Mahajan, Pramod B.
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and Its Uses

<130> 5718-34, 035718-174234

<140>

<141>

<150> 60/072,785

<151> 1998-01-27

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2949

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(2949)

<400> 1
atg gcg gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg 48
Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15
cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
20 25 30
cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45
atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60
tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct	288
Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser	
85 90 95	
aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc	336
Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala	
100 105 110	
cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tgc gtc	384
Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val	
115 120 125	
cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg	432
Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp	
130 135 140	
tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag	480
Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu	
145 150 155 160	
aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg	528
Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met	
165 170 175	
ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt	576
Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly	
180 185 190	
tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc	624
Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala	
195 200 205	
agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa	672
Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln	
210 215 220	
ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta	720
Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu	
225 230 235 240	
aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt	768
Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu	
245 250 255	
aag act cat gta tgc gct gct gaa tta agg gat atg ctt gag gct aat	816
Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn	
260 265 270	

ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg 864
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285

gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat 912
 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
 290 295 300

ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca 960
 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320

gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag 1008
 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335

aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag 1056
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350

tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca 1104
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365

atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg 1152
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380

ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa 1200
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400

tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt 1248
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
 405 410 415

gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca 1296
 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430

tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg 1344
 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
 435 440 445

ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa 1392
 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
 450 455 460

aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag	1440
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu	
465 470 475 480	
tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct	1488
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala	
485 490 495	
tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra	1536
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa	
500 505 510	
gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn	1584
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa	
515 520 525	
cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat	1632
His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp	
530 535 540	
gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt	1680
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser	
545 550 555 560	
gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca	1728
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala	
565 570 575	
atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg	1776
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp	
580 585 590	
gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt	1824
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe	
595 600 605	
tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aaa	1872
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys	
610 615 620	
gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc	1920
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu	
625 630 635 640	
atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa	1968
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu	
645 650 655	

ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra	2016
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa	
660 665 670	
aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt	2064
Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe	
675 680 685	
gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg	2112
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu	
690 695 700	
ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc	2160
Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu	
705 710 715 720	
ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt	2208
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu	
725 730 735	
gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat	2256
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp	
740 745 750	
agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt	2304
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys	
755 760 765	
gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag	2352
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu	
770 775 780	
cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tgg ctg	2400
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu	
785 790 795 800	
gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag	2448
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys	
805 810 815	
tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac	2496
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His	
820 825 830	
ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga	2544
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg	
835 840 845	

att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc 2592
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
850 855 860

ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg 2640
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
865 870 875 880

gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta 2688
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
885 890 895

gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca 2736
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
900 905 910

aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
915 920 925

tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
930 935 940

ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
945 950 955 960

atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
965 970 975

cgt ttc cat cac aag agg tag 2949
Arg Phe His His Lys Arg
980

<210> 2

<211> 982

<212> PRT

<213> Zea mays

<400> 2

Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu

20

25

30

Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
85 90 95

Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
100 105 110

Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
115 120 125

Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
130 135 140

Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
145 150 155 160

Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
165 170 175

Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
180 185 190

Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
195 200 205

Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
210 215 220

Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
225 230 235 240

Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
245 250 255

Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
260 265 270

Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala

275

280

285

Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
290 295 300

Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
305 310 315 320

Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
325 330 335

Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
340 345 350

Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
355 360 365

Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
370 375 380

Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
385 390 395 400

Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
405 410 415

Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
420 425 430

Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
435 440 445

Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
450 455 460

Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
465 470 475 480

Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
485 490 495

Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
500 505 510

Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
515 520 525

His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp

530

535

540

Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
545 550 555 560

Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
565 570 575

Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
580 585 590

Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
595 600 605

Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
610 615 620

Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
625 630 635 640

Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
645 650 655

Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
660 665 670

Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
675 680 685

Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
690 695 700

Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
705 710 715 720

Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
725 730 735

Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
740 745 750

Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
755 760 765

Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
770 775 780

Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu

785	790	795	800
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys	805	810	815
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His	820	825	830
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg	835	840	845
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly	850	855	860
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val	865	870	875
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu	885	890	895
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro	900	905	910
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu	915	920	925
Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys	930	935	940
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr	945	950	955
Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val	965	970	975
Arg Phe His His Lys Arg	980		

<210> 3

<211> 474

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(474)

<400> 3
 aac aag atg cta tta tgg cac ggt tca agg ttg acg aat ttt gtg gga 48
 Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
 1 5 10 15
 att ctt agt caa ggg cta aga att gca cct cct gag gca cct gtt act 96
 Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
 20 25 30
 ggc tat atg ttc ggc aaa ggc ctc tac ttt gca gat cta gta agc aag 144
 Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
 35 40 45
 agc gca caa tac tgt tat gtg gat agg aat aat cct gta ggt ttg atg 192
 Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60
 ctt ctt tct gag gtt gct tta gga gac atg tat gaa cta aag aaa gcc 240
 Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80
 acg tcc atg gac aaa cct cca aga ggg aag cat tcg acc aag gga tta 288
 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95
 ggc aaa acc gtg cca ctg gag tca gag ttt gtg aag tgg agg gat gat 336
 Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110
 gtc gta gtt ccc tgc ggc aag ccg gtg cca tca tca att agg agc tct 384
 Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
 115 120 125
 gaa ctc atg tac aat gag tac atc gtc tac aac aca tcc cag gtg aag 432
 Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
 130 135 140
 atg cag ttc ttg ctg aag gtg cgt ttc cat cac aag agg tag 474
 Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
 145 150 155

<210> 4
 <211> 157
 <212> PRT
 <213> Zea mays

<400> 4

Asn Lys Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly
 1 5 10 15

Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr
 20 25 30

Gly Tyr Met Phe Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys
 35 40 45

Ser Ala Gln Tyr Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met
 50 55 60

Leu Leu Ser Glu Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala
 65 70 75 80

Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
 85 90 95

Gly Lys Thr Val Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp
 100 105 110

Val Val Val Pro Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser
 115 120 125

Glu Leu Met Tyr Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys
 130 135 140

Met Gln Phe Leu Leu Lys Val Arg Phe His His Lys Arg
 145 150 155

<210> 5

<211> 530

<212> DNA

<213> Zea mays

<400> 5

ctcgtgcaag tcatgccggt ccctatcgc caaggaccag ctccgtcttg gcaagatggt 60

tcaggcgctca cagttcgagc gtttcagcc gatgtggaac catgccaggt gcattctcag 120

caagaagaac cagataaaat ccgttgacga tgttgaaggg atagatgcac ttatagtgga 180

tgatcaagag aagatacgaa actacgttgg gactgcctca gctggtacaa gttctacagc 240

tgctcctcct gagaaatgta caattgagat tgctccatct gcccgtaatt catgtagagc 300

atgcagtga aagattacaa aaggatcggt ccgtctttca gctaagcttg agagtgaagg 360

tcccaagggt ataccatggt atcatgccaa ctgtttcttt gaggtatccc cgtotgcaac 420

tgttgagaag ttctcaggct gggatacttt gtcogatgag gataagagaa ccatgctcga 480

tottgttaaa aaagatggtg gcaacaatga acaaaaataag ggtccaagc 530